

AMENDMENTS TO THE CLAIMS

1. **(Previously Presented)** A substantially pure polypeptide selected from the group consisting of a short peptide of at least seven consecutive amino acids and at most 10 consecutive amino acids, an oligopeptide of at least 11 consecutive amino acids and at most 100 consecutive amino acids and a longer polypeptide of at least 101 consecutive amino acids and at most 150 consecutive amino acids, wherein said substantially pure polypeptide comprises

- a) an amino acid sequence encoded by a member of the *esat-6* gene family,
- b) or comprises an amino acid analogue having a sequence identity with a polypeptide encoded by a member of the *esat-6* gene family of at least 94%,

wherein b) is immunologically equivalent to the polypeptide encoded by a member of the *esat-6* gene family, with the proviso that the substantially pure polypeptide is not selected from the group consisting of Rv0287, Rv0288, Rv1037c, Rv1038c, Rv1197, Rv1198, Rv1792, Rv1793, Rv2346c, Rv2347c, Rv3019c, Rv3619c, Rv3620c, Rv3874, and Rv3875.

2. **(Previously Presented)** A substantially pure polypeptide selected from the group consisting of a short peptide of at least seven consecutive amino acids and at most 10 consecutive amino acids, an oligopeptide of at least 11 consecutive amino acids and at most 100 consecutive amino acids and a longer polypeptide of at least 101 consecutive amino acids and at most 150 consecutive amino acids, wherein said substantially pure polypeptide comprises

- a) the amino acid sequence set forth in SEQ ID NOs: 7, 13, 15, 17, 19, 21, 23, 25, 27, 29 or 31 or comprises,
- b) an amino acid sequence analogue having a sequence identity with a polypeptide selected from the group consisting of SEQ ID NOs: 7, 13, 15, 17, 19, 21, 23, 25, 27, 29 and 31 of at least 70%,

wherein b) is immunologically equivalent to the polypeptide selected from the group consisting of SEQ ID NOs: 7, 13, 15, 17, 19, 21, 23, 25, 27, 29 and 31.

3. **(Previously Presented)** A substantially pure polypeptide selected from the group consisting of a short peptide of at least seven consecutive amino acids and at most 10 consecutive amino acids, an oligopeptide of at least 11 consecutive amino acids and at most 100 consecutive amino acids and a longer polypeptide of at least 101 consecutive amino acids and at most 150 amino acids, wherein said substantially pure polypeptide comprises
- a) a T-cell epitope of the amino acid sequence set forth in SEQ ID NOs: 7, 13, 15, 17, 19, 21, 23, 25, 27, 29 or 31,
 - b) or has a sequence identity of at least 70% with a T-cell epitope of the amino acid sequence set forth in a) and is immunologically equivalent to said polypeptide.
4. **(Currently Amended)** The polypeptide according to any one of the preceding claims in essentially pure form.
5. **(Previously Presented)** The polypeptide according to claim 1, which has a length of at least 7 consecutive amino acid residues, such as at least 8, at least 9, at least 10, at least 12, at least 14, at least 16, at least 18, at least 20, at least 22, at least 24, and at least 30 consecutive amino acid residues.
6. **(Previously Presented)** The polypeptide according to claim 1 which is free from any signal sequence.
7. **(Previously Presented)** A polypeptide according to claim 1, wherein said sequence identity is at least 95%.
8. **(Previously Presented)** A fusion polypeptide comprising at least one polypeptide according to claim 1 and at least one fusion partner.
9. **(Previously Presented)** A fusion polypeptide according to claim 8, wherein the fusion partner is selected from the group consisting of a polypeptide as defined in any one of claims 1-3

and 5-7, and another polypeptide from a bacterium belonging to the tuberculosis complex, such as ESAT-6 or at least one T-cell epitope thereof, TB10.4 or at least one T-cell epitope thereof, and MPT59 or at least one T-cell epitope thereof.

10. **(Previously Presented)** A fusion polypeptide according to claim 8, wherein the fusion partner is selected from the group consisting of DnaK, GroEL, urease, glutamine synthetase, L-alanine dehydrogenase, phosphate binding protein, Ag 85 complex, HBHA (heparin binding hemagglutinin), MPT51, superoxide dismutase, α -crystallin, GroES, and MPT59.

11. **(Original)** A polypeptide according to claim 1 which is lipidated so as to allow a self-adjuvating effect of the polypeptide.

12. **(Canceled)**

13. **(Canceled)**

14. **(Previously Presented)** An immunologic composition comprising at least one polypeptide according to claim 1.

15. **(Original)** An immunologic composition according to claim 14, which further comprises an immunologically and pharmaceutically acceptable carrier, vehicle or adjuvant.

16. **(Original)** An immunologic composition according to claim 15, wherein the carrier is selected from the group consisting of a polymer to which the polypeptide(s) is/are bound by hydrophobic non-covalent interaction, such as a plastic, e.g. polystyrene, a polymer to which the polypeptide(s) is/are covalently bound, such as a polysaccharide, and a polypeptide, e.g. bovine serum albumin, ovalbumin or keyhole limpet hemocyanin; the vehicle is selected from the group consisting of a diluent and a suspending agent; and the adjuvant is selected from the group consisting of dimethyldioctadecylammonium bromide (DDA), Quil A, poly I:C, Freund's

incomplete adjuvant, IFN- γ , IL-2, IL-12, monophosphoryl lipid A (MPL), and muramyl dipeptide (MDP).

17. **(Currently Amended)** An immunologic composition according to any one of claims 14-16, comprising at least two of said polypeptides.

18. **(Previously Presented)** An immunologic composition according to claim 17, comprising 3-20 of said polypeptides.

19.- 26. **(Canceled)**

27. **(Previously Presented)** A composition for diagnosing tuberculosis in an animal, including a human being, comprising a polypeptide according to claim 1.

28.- 45. **(Cancelled)**

46. **(Previously Presented)** A polypeptide according to claim 1, wherein said sequence identity is at least 96%.

47. **(Previously Presented)** A polypeptide according to claim 1, wherein said sequence identity is at least 97%.

48. **(Previously Presented)** A polypeptide according to claim 1, wherein said sequence identity is at least 98%.

49. **(Previously Presented)** A polypeptide according to claim 1, wherein said sequence identity is at least 99%.

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50. **(Previously Presented)** A polypeptide according to claim 1, wherein said sequence identity is 100%.

51. **(Canceled)**